

EXHIBIT A

1. SEQ5 vs. SEQ2

Aligned Length = 81 Gaps = 1
Identities = 45 (55%) Similarities = 12 (14%)

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SEQ5   1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ2   1 MRLALSGLLCMLLLCFCIFSSEGRHPAKSLKLR--CCHLSPRSKLT 47
      **** ** ***.*****.***.***.***.  **   ***  *   *

SEQ5   51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ2   48 TWKGNHTRPCRLCRNKLPVKS WVVP GALPQI 78
      . **.* * * . * . *****.
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2. SEQ5 vs. SEQ7

Aligned Length = 81 Gaps = 2
Identities = 38 (46%) Similarities = 11 (13%)

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SEQ5   1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ7   1 MRLTL SGLFFMLFLCLCVLSSEGRKRP AKFPKLRP---RCHLSPRSKPI 47
      **** ** * . * ** .. *.***.*****  *   **  *

SEQ5   51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ7   48 TWKGNHTRPCRPCR-KLESNS WVVP GALPQI 77
      . **.* * * *.** . * *****.
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